<110> Tryggvason, Karl
       Salo, Sirpa

<120> Use of antibodies to the gamma 2 chain of laminin 5 to inhibit tumor growth
and metastasis

<130> 02-1147-US

<150> 60/422,009
<151> 2002-10-29

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Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu
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Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly
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Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His
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Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg
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Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys
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Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg
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Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys
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Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala
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Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala
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Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu
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gat ggg ggg aac cct gag ggc tgt acc cag tgt ttc tgc tat ggg cat      693
Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His
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Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr
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Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn
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agc tca gcc caa cga cta gat cct gtc tat ttt gtg gct cct gcc aaa      885
Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys
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Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp
            260                 265                 270

tac cgt gtg gac aga gga ggc aga cac cca tct gcc cat gat gtg atc      981
Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile
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ctg gaa ggt gct ggt cta cgg atc aca gct ccc ttg atg cca ctt ggc      1029
Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly
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Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn
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gag cat cca agc aat aat tgg agc ccc cag ctg agt tac ttt gag tat      1125
Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr
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cga agg tta ctg cgg aat ctc aca gcc ctc cgc atc cga gct aca tat      1173
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Page 2

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Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala
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cgc cct gtc tct gga gcc cca gca ccc tgg gtt gaa cag tgt ata tgt    1269
Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys
        370                      375                      380

cct gtt ggg tac aag ggg caa ttc tgc cag gat tgt gct tct ggc tac    1317
Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr
385                      390                      395                      400

aag aga gat tca gcg aga ctg ggg cct ttt ggc acc tgt att cct tgt    1365
Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys
                        405                      410                      415

aac tgt caa ggg gga ggg gcc tgt gat cca gac aca gga gat tgt tat    1413
Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr
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Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly
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ttc tac aac gat ccg cac gac ccc cgc agc tgc aag cca tgt ccc tgt    1509
Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys
        450                      455                      460

cat aac ggg ttc agc tgc tca gtg att ccg gag acg gag gag gtg gtg    1557
His Asn Gly Phe Ser Cys Ser Val Ile Pro Glu Thr Glu Glu Val Val
465                      470                      475                      480

tgc aat aac tgc cct ccc ggg gtc acc ggt gcc cgc tgt gag ctc tgt    1605
Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys
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gct gat ggc tac ttt ggg gac ccc ttt ggt gaa cat ggc cca gtg agg    1653
Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg
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cct tgt cag ccc tgt caa tgc aac agc aat gtg gac ccc agt gcc tct    1701
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ggg aat tgt gac cgg ctg aca ggc agg tgt ttg aag tgt atc cac aac    1749
Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn
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aca gcc ggc atc tac tgc gac cag tgc aaa gca ggc tac ttc ggg gac    1797
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cca ttg gct ccc aac cca gca gac aag tgt cga gct tgc aac tgt aac    1845
Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn
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ccc atg ggc tca gag cct gta gga tgt cga agt gat ggc acc tgt gtt    1893
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Gln Gln Leu Gln Arg Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly
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Asp Gly Val Val Pro Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala
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gag cag gcc ctt cag gac att ctg aga gat gcc cag att tca gaa ggt    2133
Glu Gln Ala Leu Gln Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly
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gct agc aga tcc ctt ggt ctc cag ttg gcc aag gtg agg agc caa gag    2181
Ala Ser Arg Ser Leu Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu
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aac agc tac cag agc cgc ctg gat gac ctc aag atg act gtg gaa aga    2229
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Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn
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ggc ttt aaa agt ctg gct cag gag gcc aca aga tta gca gaa agc cac    2421
Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His
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Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp
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tat tcc aaa caa gcc ctc tca ctg gtg cgc aag gcc ctg cat gaa gga    2517
Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly
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tcc ttt cag gtg gaa gaa gca aag agg atc aaa caa aaa gcg gat tca      2757
Ser Phe Gln Val Glu Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser
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ctc tca agc ctg gta acc agg cat atg gat gag ttc aag cgt aca caa      2805
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Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu
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cag gtg gac aac aga aaa gca gaa gct gaa gaa gcc atg aag aga ctc      3045
Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu
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gcc ttg gcc atg gaa aag gga ctg gcc tct ctg aag agt gag atg          3276
Ala Leu Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met
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agg gaa gtg gaa gga gag ctg gaa agg aag gag ctg gag ttt gac          3321
Arg Glu Val Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp
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acg aat atg gat gca gta cag atg gtg att aca gaa gcc cag aag          3366
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Page 5

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Ser Val Asp Glu Glu Gly Leu Val Leu Leu Glu Gln Lys Leu Ser
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ctg gag aca agc ata gat ggg att ctg gct gat gtg aag aac ttg          3636
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Glu Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys Tyr Asn Thr Gln
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Page 6

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65                  70                  75                  80


Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys
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Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg
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Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys
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Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala
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Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His
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Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn
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Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe
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Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn
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Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr
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Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr
            340             345             350

Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala
            355             360             365

Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys
    370             375             380

Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr
385             390             395             400

Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys
            405             410             415
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Page 8

Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr
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Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly
            435   440   445

Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys
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His Asn Gly Phe Ser Cys Ser Val Ile Pro Glu Thr Glu Glu Val Val
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Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys
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            500   505   510

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Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His
        755   760   765

Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp
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Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly
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Val Gly Ser Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu
                805   810   815

Val Glu Lys Leu Glu Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg
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Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser
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Leu Arg Leu Leu Asp Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln
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Ser Phe Gln Val Glu Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser
865   870   875   880

Leu Ser Ser Leu Val Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln
                885   890   895

Lys Asn Leu Gly Asn Trp Lys Glu Glu Ala Gln Gln Leu Leu Gln Asn
        900   905   910

Page 10

Gly Lys Ser Gly Arg Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn
    915   920   925

Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr
    930   935   940

Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu
945   950   955   960

Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu
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Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln
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Glu Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly
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Ala Leu Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met
    1040   1045   1050

Arg Glu Val Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp
    1055   1060   1065

Thr Asn Met Asp Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys
    1070   1075   1080

Val Asp Thr Arg Ala Lys Asn Ala Gly Val Thr Ile Gln Asp Thr
    1085   1090   1095

Leu Asn Thr Leu Asp Gly Leu Leu His Leu Met Asp Gln Pro Leu
    1100   1105   1110

Ser Val Asp Glu Glu Gly Leu Val Leu Leu Glu Gln Lys Leu Ser
    1115   1120   1125

Arg Ala Lys Thr Gln Ile Asn Ser Gln Leu Arg Pro Met Met Ser
    1130   1135   1140

Glu Leu Glu Glu Arg Ala Arg Gln Gln Arg Gly His Leu His Leu
    1145   1150   1155

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Leu Glu  Thr Ser Ile Asp Gly  Ile Leu Ala Asp Val  Lys Asn Leu
    1160                 1165             1170

Glu Asn  Ile Arg Asp Asn Leu  Pro Pro Gly Cys Tyr  Asn Thr Gln
    1175                 1180             1185

Ala Leu  Glu Gln Gln
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atg cct gcg ctc tgg ctg ggc tgc tgc ctc tgc ttc tcg ctc ctc ctg       165
Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu
1                   5                  10                  15

ccc gca gcc cgg gcc acc tcc agg agg gaa gtc tgt gat tgc aat ggg       213
Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly
                20                  25                  30

aag tcc agg cag tgt atc ttt gat cgg gaa ctt cac aga caa act ggt       261
Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly
            35                  40                  45

aat gga ttc cgc tgc ctc aac tgc aat gac aac act gat ggc att cac       309
Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His
        50                  55                  60

tgc gag aag tgc aag aat ggc ttt tac cgg cac aga gaa agg gac cgc       357
Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg
65                  70                  75                  80
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tgt ttg ccc tgc aat tgt aac tcc aaa ggt tct ctt agt gct cga tgt      405
Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys
                85                  90                  95

gac aac tct gga cgg tgc agc tgt aaa cca ggt gtg aca gga gcc aga      453
Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg
                100                 105                 110

tgc gac cga tgt ctg cca ggc ttc cac atg ctc acg gat gcg ggg tgc      501
Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys
            115                 120                 125

acc caa gac cag aga ctg cta gac tcc aag tgt gac tgt gac cca gct      549
Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala
        130                 135                 140

ggc atc gca ggg ccc tgt gac gcg ggc cgc tgt gtc tgc aag cca gct      597
Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala
145                 150                 155                 160

gtt act gga gaa cgc tgt gat agg tgt cga tca ggt tac tat aat ctg      645
Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu
                165                 170                 175

gat ggg ggg aac cct gag ggc tgt acc cag tgt ttc tgc tat ggg cat      693
Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His
            180                 185                 190

tca gcc agc tgc cgc agc tct gca gaa tac agt gtc cat aag atc acc      741
Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr
            195                 200                 205

tct acc ttt cat caa gat gtt gat ggc tgg aag gct gtc caa cga aat      789
Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn
        210                 215                 220

ggg tct cct gca aag ctc caa tgg tca cag cgc cat caa gat gtg ttt      837
Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe
225                 230                 235                 240

agc tca gcc caa cga cta gat cct gtc tat ttt gtg gct cct gcc aaa      885
Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys
                245                 250                 255

ttt ctt ggg aat caa cag gtg agc tat ggg caa agc ctg tcc ttt gac      933
Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp
            260                 265                 270

tac cgt gtg gac aga gga ggc aga cac cca tct gcc cat gat gtg atc      981
Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile
        275                 280                 285

ctg gaa ggt gct ggt cta cgg atc aca gct ccc ttg atg cca ctt ggc      1029
Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly
        290                 295                 300

aag aca ctg cct tgt ggg ctc acc aag act tac aca ttc agg tta aat      1077
Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn
305                 310                 315                 320

gag cat cca agc aat aat tgg agc ccc cag ctg agt tac ttt gag tat      1125
Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr
            325                 330                 335
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cga agg tta ctg cgg aat ctc aca gcc ctc cgc atc cga gct aca tat        1173
Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr
        340             345             350

gga gaa tac agt act ggg tac att gac aat gtg acc ctg att tca gcc        1221
Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala
        355             360             365

cgc cct gtc tct gga gcc cca gca ccc tgg gtt gaa cag tgt ata tgt        1269
Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys
370             375             380

cct gtt ggg tac aag ggg caa ttc tgc cag gat tgt gct tct ggc tac        1317
Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr
385             390             395             400

aag aga gat tca gcg aga ctg ggg cct ttt ggc acc tgt att cct tgt        1365
Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys
        405             410             415

aac tgt caa ggg gga ggg gcc tgt gat cca gac aca gga gat tgt tat        1413
Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr
        420             425             430

tca ggg gat gag aat cct gac att gag tgt gct gac tgc cca att ggt        1461
Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly
        435             440             445

ttc tac aac gat ccg cac gac ccc cgc agc tgc aag cca tgt ccc tgt        1509
Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys
        450             455             460

cat aac ggg ttc agc tgc tca gtg att ccg gag acg gag gag gtg gtg        1557
His Asn Gly Phe Ser Cys Ser Val Ile Pro Glu Thr Glu Glu Val Val
465             470             475             480

tgc aat aac tgc cct ccc ggg gtc acc ggt gcc cgc tgt gag ctc tgt        1605
Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys
        485             490             495

gct gat ggc tac ttt ggg gac ccc ttt ggt gaa cat ggc cca gtg agg        1653
Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg
        500             505             510

cct tgt cag ccc tgt caa tgc aac agc aat gtg gac ccc agt gcc tct        1701
Pro Cys Gln Pro Cys Gln Cys Asn Ser Asn Val Asp Pro Ser Ala Ser
        515             520             525

ggg aat tgt gac cgg ctg aca ggc agg tgt ttg aag tgt atc cac aac        1749
Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn
        530             535             540

aca gcc ggc atc tac tgc gac cag tgc aaa gca ggc tac ttc ggg gac        1797
Thr Ala Gly Ile Tyr Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp
545             550             555             560

cca ttg gct ccc aac cca gca gac aag tgt cga gct tgc aac tgt aac        1845
Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn
        565             570             575

ccc atg ggc tca gag cct gta gga tgt cga agt gat ggc acc tgt gtt        1893
Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val
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Page 14

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                  580                        585                      590
tgc aag cca gga ttt ggt ggc ccc aac tgt gag cat gga gca ttc agc      1941
Cys Lys Pro Gly Phe Gly Gly Pro Asn Cys Glu His Gly Ala Phe Ser
        595                 600                 605

tgt cca gct tgc tat aat caa gtg aag att cag atg gat cag ttt atg      1989
Cys Pro Ala Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met
        610                 615                 620

cag cag ctt cag aga atg gag gcc ctg att tca aag gct cag ggt ggt      2037
Gln Gln Leu Gln Arg Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly
625                 630                 635                 640

gat gga gta gta cct gat aca gag ctg gaa ggc agg atg cag cag gct      2085
Asp Gly Val Val Pro Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala
                645                 650                 655

gag cag gcc ctt cag gac att ctg aga gat gcc cag att tca gaa ggt      2133
Glu Gln Ala Leu Gln Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly
                660                 665                 670

gct agc aga tcc ctt ggt ctc cag ttg gcc aag gtg agg agc caa gag      2181
Ala Ser Arg Ser Leu Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu
                675                 680                 685

aac agc tac cag agc cgc ctg gat gac ctc aag atg act gtg gaa aga      2229
Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg
        690                 695                 700

gtt cgg gct ctg gga agt cag tac cag aac cga gtt cgg gat act cac      2277
Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His
705                 710                 715                 720

agg ctc atc act cag atg cag ctg agc ctg gca gaa agt gaa gct tcc      2325
Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser
                725                 730                 735

ttg gga aac act aac att cct gcc tca gac cac tac gtg ggg cca aat      2373
Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn
                740                 745                 750

ggc ttt aaa agt ctg gct cag gag gcc aca aga tta gca gaa agc cac      2421
Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His
        755                 760                 765

gtt gag tca gcc agt aac atg gag caa ctg aca agg gaa act gag gac      2469
Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp
        770                 775                 780

tat tcc aaa caa gcc ctc tca ctg gtg cgc aag gcc ctg cat gaa gga      2517
Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly
785                 790                 795                 800

gtc gga agc gga agc ggt agc ccg gac ggt gct gtg gtg caa ggg ctt      2565
Val Gly Ser Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu
                805                 810                 815

gtg gaa aaa ttg gag aaa acc aag tcc ctg gcc cag cag ttg aca agg      2613
Val Glu Lys Leu Glu Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg
                820                 825                 830

gag gcc act caa gcg gaa att gaa gca gat agg tct tat cag cac agt      2661
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Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser
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ctc cgc ctc ctg gat tca gtg tct ccg ctt cag gga gtc agt gat cag    2709
Leu Arg Leu Leu Asp Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln
    850             855                 860

tcc ttt cag gtg gaa gaa gca aag agg atc aaa caa aaa gcg gat tca    2757
Ser Phe Gln Val Glu Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser
865             870                 875                 880

ctc tca agc ctg gta acc agg cat atg gat gag ttc aag cgt aca caa    2805
Leu Ser Ser Leu Val Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln
                885             890                 895

aag aat ctg gga aac tgg aaa gaa gaa gca cag cag ctc tta cag aat    2853
Lys Asn Leu Gly Asn Trp Lys Glu Glu Ala Gln Gln Leu Leu Gln Asn
            900             905                 910

gga aaa agt ggg aga gag aaa tca gat cag ctg ctt tcc cgt gcc aat    2901
Gly Lys Ser Gly Arg Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn
            915             920                 925

ctt gct aaa agc aga gca caa gaa gca ctg agt atg ggc aat gcc act    2949
Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr
    930             935                 940

ttt tat gaa gtt gag agc atc ctt aaa aac ctc aga gag ttt gac ctg    2997
Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu
945             950                 955                 960

cag gtg gac aac aga aaa gca gaa gct gaa gaa gcc atg aag aga ctc    3045
Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu
                965             970                 975

tcc tac atc agc cag aag gtt tca gat gcc agt gac aag acc cag caa    3093
Ser Tyr Ile Ser Gln Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln
            980             985                 990

gca gaa aga gcc ctg ggg agc gct gct gct gat gca cag agg gca aag   3141
Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys
        995             1000                1005

aat ggg gcc ggg gag gcc ctg gaa atc tcc agt gag att gaa cag       3186
Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln
    1010            1015                1020

gag att ggg agt ctg aac ttg gaa gcc aat gtg aca gca gat gga       3231
Glu Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly
    1025            1030                1035

gcc ttg gcc atg gaa aag gga ctg gcc tct ctg aag agt gag atg       3276
Ala Leu Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met
    1040            1045                1050

agg gaa gtg gaa gga gag ctg gaa agg aag gag ctg gag ttt gac       3321
Arg Glu Val Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp
    1055            1060                1065

acg aat atg gat gca gta cag atg gtg att aca gaa gcc cag aag       3366
Thr Asn Met Asp Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys
    1070            1075                1080
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gtt gat  acc aga gcc aag aac  gct ggg gtt aca atc  caa gac aca      3411
Val Asp  Thr Arg Ala Lys Asn  Ala Gly Val Thr Ile  Gln Asp Thr
    1085             1090               1095

ctc aac  aca tta gac ggc ctc  ctg cat ctg atg ggt  atg tga          3453
Leu Asn  Thr Leu Asp Gly Leu  Leu His Leu Met Gly  Met
    1100             1105               1110
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acccacaacc cacaaccttc cagctccatg ctccagggct ttgctccaga acactcacta   3513

tacctagccc cagcaaaggg gagtctcagc tttccttaag gatatcagta aatgtgcttt   3573

gtttccaggc ccagataact ttcggcaggt tcccttacat ttactggacc ctgttttacc   3633

gttgctaaga tgggtcactg aacacctatt gcacttgggg gtaaaggtct gtgggccaaa   3693

gaacaggtgt atataagcaa cttcacagaa cacgagacag cttgggaatc ctgctaaaga   3753

gtctggcctg accctgaga agccagtgga cagttttaag cagaggaata acatcaccac    3813

tgtatatttc agaaagatca ctagggcagc cgagtggagg aaagcttgaa gaggggggtta  3873

gagagaaggc aggttgagac tacttaagat attgttgaaa taattgaaga gagaaatgac   3933

aggagcctgc tctaaggcag tagaatggtg gctgggaaga tgtgaaggaa gattttccca   3993

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cactttggga gactgaagcg ggtggatcac ccgaggtcag gagttgaaga ccagcctggc   4113

caacatggtg aaaccctgtc tctactaaaa gtacaaaaat tagctggatg atggtggtgg   4173

gcgcctgtaa ttccagctac tcaggagtct gaggcaggag aatcgcttga acccaggagg   4233

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cctaaaaaaa aaaaaaaaaa aaa                                           4316
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Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly
            20              25              30


Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly
        35              40              45


Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His
    50              55              60


Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg
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Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys
                85   90   95

Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg
            100   105   110

Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys
        115   120   125

Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala
    130   135   140

Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala
145   150   155   160

Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu
            165   170   175

Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His
            180   185   190

Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr
        195   200   205

Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn
    210   215   220

Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe
225   230   235   240

Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys
            245   250   255

Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp
            260   265   270

Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile
        275   280   285

Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly
    290   295   300

Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn
305   310   315   320

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Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr
            325             330                 335


Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr
            340             345                 350


Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala
            355             360                 365


Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys
    370             375             380


Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr
385             390             395                 400


Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys
            405             410                 415


Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr
            420             425                 430


Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly
            435             440                 445


Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys
    450             455             460


His Asn Gly Phe Ser Cys Ser Val Ile Pro Glu Thr Glu Glu Val Val
465             470             475                 480


Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys
            485             490                 495


Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg
            500             505                 510


Pro Cys Gln Pro Cys Gln Cys Asn Ser Asn Val Asp Pro Ser Ala Ser
            515             520             525


Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn
    530             535             540


Thr Ala Gly Ile Tyr Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp
545             550             555                 560


Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn
            565             570                 575
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Page 19

Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val
            580   585   590

Cys Lys Pro Gly Phe Gly Gly Pro Asn Cys Glu His Gly Ala Phe Ser
        595   600   605

Cys Pro Ala Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met
    610   615   620

Gln Gln Leu Gln Arg Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly
625   630   635   640

Asp Gly Val Val Pro Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala
            645   650   655

Glu Gln Ala Leu Gln Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly
        660   665   670

Ala Ser Arg Ser Leu Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu
    675   680   685

Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg
    690   695   700

Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His
705   710   715   720

Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser
            725   730   735

Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn
            740   745   750

Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His
        755   760   765

Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp
    770   775   780

Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly
785   790   795   800

Val Gly Ser Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu
            805   810   815

Val Glu Lys Leu Glu Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg
            820   825   830

Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser
        835   840   845

Leu Arg Leu Leu Asp Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln
    850   855   860

Ser Phe Gln Val Glu Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser
865   870   875   880

Leu Ser Ser Leu Val Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln
            885   890   895

Lys Asn Leu Gly Asn Trp Lys Glu Glu Ala Gln Gln Leu Leu Gln Asn
        900   905   910

Gly Lys Ser Gly Arg Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn
        915   920   925

Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr
    930   935   940

Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu
945   950   955   960

Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu
            965   970   975

Ser Tyr Ile Ser Gln Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln
        980   985   990

Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys
        995   1000   1005

Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln
    1010   1015   1020

Glu Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly
    1025   1030   1035

Ala Leu Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met
    1040   1045   1050

Arg Glu Val Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp
    1055   1060   1065

Thr Asn Met Asp Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys
Page 21

```
              1070                1075               1080
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Val Asp  Thr Arg Ala Lys Asn  Ala Gly Val Thr Ile  Gln Asp Thr
         1085                1090               1095
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Leu Asn  Thr Leu Asp Gly Leu  Leu His Leu Met Gly  Met
         1100                1105               1110
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gttattcagg ggatgagaat cctgacattg agtgtgctga ctgcccaatt ggtttctaca    180

acgatccgca cgaccccgc agctgcaagc catgtccctg tcataacggg ttcagctgct     240

cagtgattcc ggagacggag gaggtggtgt gcaataactg ccctcccggg gtcaccggtg    300

cccgctgtga gctctgtgct gatggctact ttggggaccc ctttggtgaa catggcccag    360

tgaggccttg tcagccctgt caatgcaaca gcaatgtgga ccccagtgcc tctgggaatt    420

gtgaccggct gacaggcagg tgtttgaagt gtatccacaa cacagccggc atctactgcg    480

accagtgcaa agcaggctac ttcggggacc cattggctcc caacccagca               530
```

```
<210>  6
<211>  177
<212>  PRT
<213>  Homo sapiens
```

```
<220>
<221>  misc_feature
<223>  Portion of Domain III of laminin gamma 2.
```

```
<400>  6
```

```
Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr Lys Arg Asp Ser Ala Arg
1               5                  10                  15
```

```
Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys Asn Cys Gln Gly Gly Gly
            20                  25                  30
```

```
Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr Ser Gly Asp Glu Asn Pro
       35                  40                  45
```

```
Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly Phe Tyr Asn Asp Pro His
    50              55              60

Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys His Asn Gly Phe Ser Cys
65              70              75              80

Ser Val Met Pro Glu Thr Glu Glu Val Val Cys Asn Asn Cys Pro Pro
            85              90              95

Gly Val Thr Gly Ala Arg Cys Glu Leu Cys Ala Asp Gly Tyr Phe Gly
            100             105             110

Asp Pro Phe Gly Glu His Gly Pro Val Arg Pro Cys Gln Pro Cys Gln
        115             120             125

Cys Asn Asn Asn Val Asp Pro Ser Ala Ser Gly Asn Cys Asp Arg Leu
    130             135             140

Thr Gly Arg Cys Leu Lys Cys Ile His Asn Thr Ala Gly Ile Tyr Cys
145             150             155             160

Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp Pro Leu Ala Pro Asn Pro
            165             170             175

Ala
```

<210> 7
<211> 681
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Complete domain III of laminin gamma 2

<400> 7
```
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agagattcag cgagactggg gccttttggc acctgtattc cttgtaactg tcaaggggga     120
ggggcctgtg atccagacac aggagattgt tattcagggg atgagaatcc tgacattgag     180
tgtgctgact gcccaattgg tttctacaac gatccgcacg accccgcag ctgcaagcca      240
tgtccctgtc ataacgggtt cagctgctca gtgattccgg agacggagga ggtggtgtgc     300
aataactgcc ctcccggggt caccggtgcc cgctgtgagc tctgtgctga tggctacttt     360
ggggacccct ttggtgaaca tggcccagtg aggccttgtc agccctgtca atgcaacagc     420
```

```
aatgtggacc ccagtgcctc tgggaattgt gaccggctga caggcaggtg tttgaagtgt    480

atccacaaca cagccggcat ctactgcgac cagtgcaaag caggctactt cggggaccca    540

ttggctccca acccagcaga caagtgtcga gcttgcaact gtaacccat gggctcagag    600

cctgtaggat gtcgaagtga tggcacctgt gtttgcaagc caggatttgg tggccccaac    660

tgtgagcatg gagcattcag c    681
```

<210> 8
<211> 227
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Complete domain III of laminin gamma 2.

<400> 8

```
Cys Ile Cys Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala
1               5                   10                  15

Ser Gly Tyr Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys
            20                  25                  30

Ile Pro Cys Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp Thr Gly
        35                  40                  45

Asp Cys Tyr Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys
    50                  55                  60

Pro Ile Gly Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro
65                  70                  75                  80

Cys Pro Cys His Asn Gly Phe Ser Cys Ser Val Met Pro Glu Thr Glu
                85                  90                  95

Glu Val Val Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys
                100                 105                 110

Glu Leu Cys Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly
            115                 120                 125

Pro Val Arg Pro Cys Gln Pro Cys Gln Cys Asn Asn Asn Val Asp Pro
        130                 135                 140

Ser Ala Ser Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys
145                 150                 155                 160
```

Page 24

```
Ile His Asn Thr Ala Gly Ile Tyr Cys Asp Gln Cys Lys Ala Gly Tyr
             165             170             175
```

```
Phe Gly Asp Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys
             180             185             190
```

```
Asn Cys Asn Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly
             195             200             205
```

```
Thr Cys Val Cys Lys Pro Gly Phe Gly Gly Pro Asn Cys Glu His Gly
    210             215             220
```

```
Ala Phe Ser
225
```

<210> 9
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> N-terminal portion of domain III of laminin gamma 2.

<400> 9

```
Cys Ile Cys Pro Val Gly Tyr Lys Gly
1               5
```

<210> 10
<211> 41
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> C-terminal portion of domain III of laminin gamma 2.

<400> 10

```
Asp Lys Cys Arg Ala Cys Asn Cys Asn Pro Met Gly Ser Glu Pro Val
1               5               10              15
```

```
Gly Cys Arg Ser Asp Gly Thr Cys Val Cys Lys Pro Gly Phe Gly Gly
             20              25              30
```

```
Pro Asn Cys Glu His Gly Ala Phe Ser
             35              40
```